MOLECULAR CHARACTERIZATION OF BANANA BUNCHY TOP VIRUS REVEALS WIDESPREAD LOW GENETIC VARIATION AMONG ISOLATES IN DEMOCRATIC REPUBLIC OF CONGO

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BACKGROUND and OBJECTIVES

Banana bunchy top virus (BBTV), is the most devastating and widespread banana virus. Banana and plantain (*Musa* spp.) are major crops in terms of household income and food security in Democratic republic of Congo (DRC) (1). Despite the large territory under banana and plantain cultivation in the country, the genetic characterization of BBTV isolates has been undertaken for two provinces. The main objectives of this work were to understand the genetic variability of DRC BBTV isolates and to determine their origin.

MATERIALS and METHODS

In this study, genetic variation in BBTV was assessed from 52 BBTV isolates collected in five out of 11 provinces in DRC (Bandundu, Bas-Congo, Katanga, Kinshasa and Kasai Oriental). 52 full sequences of DNA-R and 30 full sequences of all BBTV components were analysed.

RESULTS

Full genome sequencing of DNA-R components was performed revealing a low genetic variation (98-100% nucleotide identity) amongst the BBTV isolates detected in seven of 11 DRC provinces. The phylogenetic tree showed that all DRC isolates gather a unique clade in the South Pacific group of BBTV. Based on the coding region for replication initiator protein, haplotype diversity was estimated to be 0.944±0.013, with 30 different haplotypes from 68 isolates in DRC. In addition, fives isolates were selected from each province for total genome sequencing, confirming low genetic variation among isolates from seven provinces (97-100% nucleotide identity).

CONCLUSION

This study strengthens the hypothesis of a single BBTV introduction some time ago, followed by the spread of the virus in the country. Analysis of the geographical dispersion reveals specific haplotypes groups according to the different agro-environmental conditions.

REFERENCES

(1) Bakelana, B. K. M., T. (1996). "La production de Bananes et Bananes plantain en République Démocratique du Congo." Infomusa: 103-112.

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